1642
#18

NOV 2 9 2001

RECEIVED

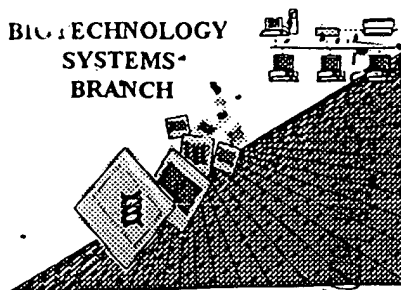# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/451739 D_

Source: _A U 1600_

Date Processed by STIC: _11/02/01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/451739

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

1. ____ Wrapped Nucleics
   Wrapped Aminos

   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2. ____ Invalid Line Length

   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3. ____ Misaligned Amino
   Numbering

   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4. ____ Non-ASCII

   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5. ____ Variable Length

   Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6. ____ PatentIn 2.0
   "bug"

   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7. ____ Skipped Sequences
   (OLD RULES)

   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   This sequence is intentionally skipped

   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8. ____ Skipped Sequences
   (NEW RULES)

   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequen
   <210> sequence id number
   <400> sequence id number
   000

9. ____ Use of n's or Xaa's
   (NEW RULES)

   Use of n's and/or Xaa's have been detected in the Sequence Listing.
   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10. ____ Invalid <213>
    Response

    Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown is Artificial Sequence

11. ____ Use of <220>

    Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12. ____ PatentIn 2.0
    "bug"

    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13. ____ Misuse of n

    n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represe any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/451,739D

DATE: 11/09/2001
TIME: 11:14:22

Input Set : A:\#703518vl -DECEMBER 8 REVISED SEQUENCE LISTING NDH.txt
Output Set: N:\CRF3\11092001\I451739D.raw

```
 1 <110> APPLICANT: Jager, Dirk
 2         Scanlan, Matthew
 3         Gure, Ali
 4         Jager, Elke
 5         Knuth, Alexander
 6         Old, Lloyd
 7         Chen, Yao-tseng
 9 <120> TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
Antigens,
10         the Antigens per se, and Uses Thereof
12 <130> FILE REFERENCE: LUD 5615
14 <140> CURRENT APPLICATION NUMBER: 09/451,739D
16 <141> CURRENT FILING DATE: 1999-11-30
18 <160> NUMBER OF SEQ ID NOS: 19
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1533
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
```

Does Not Comply
Corrected Diskette Needer

(handwritten annotations: Errored, Field 220, 223, 222, Errors?, Page 5 of 7 β)

```
W-->  25 <220> FEATURE:
      26 <221> NAME/KEY: CDS
      27 <222> LOCATION: 235
      28 <223> OTHER INFORMATION: unknown
W-->  29 <400> SEQUENCE: 1
      30 ggttttccac gttggacaag tgcggctcgg cggccagcgg agcgcgcccc ttcccgctgc   60
      32 ccgctccgct cctctcttct acccagccca gtgggcgagt gggcagcggc ggccgcggcg  120
      34 ctgggccctc tcccgccggt gtgtgcgcgc tcgtacgcgc ggcccccggc gccagccccg  180
W-->  36 ccgcctgaga gggggcctgc gccgccggcc ggggcgtgcg cccgggagcc accgcaccg   240
      38 cggcccgcgc cctcaggcgc tggggtcccc gcggacccgg aggcggcgga cgggctcggc  300
      40 agatgtagcc gccgggccga agcaggagcc ggcggggggg cgccgggaga gcgagggctt  360
      42 tgcattttgc agtgctattt tttgagggggg cggagggtg gaggaagtcg gaaagccgcg  420
      44 ccgagtcgcc ggggacctcc ggggtgaacc atgttgagtc ctgccaacgg ggagcagctc  480
      46 cacctggtga actatgtgga ggactacctg gactccatcg agtccctgcc tttcgacttg  540
      48 cagagaaatg tctcgctgat gcgggagatc gacgcgaaat accaagagat cctgaaggag  600
      50 ctagacgagt gctacgagcg cttcagtcgc gagacagacg gggcgcagaa gcggcggatg  660
      52 ctgcactgtg tgcagcgcgc gctgatccgc agccaggagc tgggcgacga gaagatccag  720
      54 atcgtgagcc agatggtgga gctggtggag aaccgcacgc ggcaggtgga cagccacgtg  780
      56 gagctgttcg aggcgcagca ggagctgggc gacacagcgg gcaacagcgg caaggctggc  840
      58 gcggacaggc ccaaaggcga ggcggcagcg caggctgaca agcccaacag caagcgctca  900
      60 cggcggcagc gcaacaacga gaaccgtgag aacgcgtcca gcaaccacga ccacgacgac  960
      62 ggcgcctcgg gcacacccaa ggagaagaag gccaagacct ccaagaagaa gaagcgctcc 1020
      64 aaggccaagg cggagcgaga ggcgtcccct gccgacctcc ccatcgaccc caacgaaccc 1080
      66 acgtactgtc tgtgcaacca ggtctcctat ggggagatga tcggctgcga caacgacgag 1140
      68 tgccccatcg agtggttcca cttctcgtgc gtggggctca atcataaacc caagggcaag 1200
      70 tggtactgtc ccaagtgccg gggggagaac gagaagacca tggacaaagc cctggagaaa 1260
      72 tccaaaaaag agagggctta caacaggtag tttgtggaca ggcgcctggt gtgaggagga 1320
      74 caaaataaac cgtgtattta ttacattgct gcctttgttg aggtgcaagg agtgtaaaat 1380
      76 gtatattttt aaagaatgtt agaaaaggaa ccattccttt cataggatg gcagtgattc 1440
      78 tgtttgcctt ttgtttttcat tggtacacgt gtaacaagaa agtggtctgt ggatcagcat 1500
```

RAW SEQUENCE LISTING   DATE: 11/09/2001
PATENT APPLICATION: US/09/451,739D   TIME: 11:14:22

Input Set : A:\#703518v1 -DECEMBER 8 REVISED SEQUENCE LISTING NDH.txt
Output Set: N:\CRF3\11092001\I451739D.raw

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       80 tttagaaact acaaatatag gtttgattca aca                              1533
       83 <210> SEQ ID NO: 2
       84 <211> LENGTH: 1143
       85 <212> TYPE: DNA
       86 <213> ORGANISM: Homo sapiens
W--> 87 <400> SEQUENCE: 2
       88 gagtaacccg ataatatgcc gttgtccggc acggcgacga gaattcccag atatagcagt   60
       90 agcagtgatc ccgggcctgt ggctcggggc cggggctgca gttcggaccg cctcccgcga  120
       92 cccgcggggg ctcggagaca gtttcaggcc gcatctttgc tgacccgagg gtggggccgc  180
       94 gcgtggccgt ggaaacagat cctgaaggag ctagacgagt gctacgagcg cttcagtcgc  240
       96 gagacagacg gggcgcagaa gcggcggatg ctgcactgtg tgcagcgcgc gctgatccgc  300
       98 agccaggagc tgggcgacga gaagatccag atcgtgagcc agatggtgga gctggtggag  360
      100 aaccgcacgc ggcaggtgga cagccacgtg gagctgttcg aggcgcagca ggagctgggc  420
      102 gacacagtgg gcaacagcgg caaggttggc gcggacaggc ccaatggcga tgcggtagcg  480
      104 cagtctgaca agcccaacag caagcgctca cggcggcagc gcaacaacga gaaccgtgag  540
      106 aacgcgtcca gcaaccacga ccacgacgac ggcgcctcgg gcacacccaa ggagaagaag  600
      108 gccaagacct ccaagaagaa gaagcgctcc aaggccaagg cggagcgaga ggcgtcccct  660
      110 gccgacctcc ccatcgaccc caacgaaccc acgtactgtc tgtgcaacca ggtctcctat  720
      112 ggggagatga tcggctgcga caacgacgag tgccccatcg agtggttcca cttctcgtgc  780
      114 gtggggctca atcataaacc caagggcaag tggtactgtc ccaagtgccg ggggggagaac  840
      116 gagaagacca tggacaaagc cctggagaaa tccaaaaaag agagggctta aacaggtag   900
      118 tttgtggaca ggcgcctggt gtgaggagga caaaataaac cgtgtattta ttacattgct  960
      120 gcctttgttg aggtgcaagg agtgtaaaat gtatattttt aaagaatgtt agaaaaggaa 1020
      122 ccattccttt cataggggatg gcagtgattc tgtttgcctt ttgtttttcat tggtacacgt 1080
      124 gtaacaagaa agtggtctgt ggatcagcat tttagaaact acaaatatag gtttgattca 1140
      126 aca                                                               1143
      129 <210> SEQ ID NO: 3
      130 <211> LENGTH: 742
      131 <212> TYPE: DNA
      132 <213> ORGANISM: Homo sapiens
W--> 133 <220> FEATURE:
W--> 134 <400> SEQUENCE: 3
      135 cgccgtccac accccagcgg ccctgacgct gtcccctccg cgaccctcgc ctctggaaaa   60
      137 agtgacaggc aaggccacgc ccccgcgagg gccggcctcg agcccgcagc ccccagggcc  120
      139 tgggacgaga tcctgaagga gctagacgag tgctacgagc gcttcagtcg cgagacagac  180
      141 ggggcgcaga agcggcggat gctgcactgt gtgcagcgcg cgctgatccg cagccaggag  240
      143 ctgggcgacg agaagatcca gatcgtgagc cagatggtgg agctggtgga gaaccgcacg  300
      145 cggcaggtgg acagccacgt ggagctgttc gaggcgcagc aggagctggg cgacacagcg  360
      147 ggcaacagcg gcaaggctgg cgcggacagg cccaaaggcg aggcggcagc gcaggctgac  420
      149 aagcccaaca gcaagcgctc acggcggcag cgcaacaacg agaaccgtga gaacgcgtcc  480
      151 agcaaccacg accacgacga cggcgcctcg ggcacaccca aggagaagaa ggccaagacc  540
      153 tccaagaaga agaagcgctc caaggccaag gcggagcgag aggcgtcccc tgccgacctc  600
      155 cccatcgacc ccaacgaacc cacgtactgt ctgtgcaacc aggtctccta tggggagatg  660
      157 atcggctgcg acaacgacga gtgccccatc gagtggttcc acttctcgtg cgtggggctc  720
      159 aatcataaac ccaagggcaa gt                                           742
      162 <210> SEQ ID NO: 4
      163 <211> LENGTH: 857
      164 <212> TYPE: DNA
      165 <213> ORGANISM: Homo sapiens
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RAW SEQUENCE LISTING   DATE: 11/09/2001
PATENT APPLICATION: US/09/451,739D   TIME: 11:14:22

Input Set : A:\#703518v1 -DECEMBER 8 REVISED SEQUENCE LISTING NDH.txt
Output Set: N:\CRF3\11092001\I451739D.raw

```
W--> 166 <400> SEQUENCE: 4
     167 cctccgagaa cggtgtccat ggcacagggc gggaagagat aaggcctagg gaaggcgccc   60
     169 ctcgggccta tccacctctt ctggggctcg gcactaggaa gcagcttccc tctcaggccc  120
     171 ctttgtctcc aagccgttcc aaactgagta ccgggagacg acacaaaggg agggcggtga  180
     173 cggatggcgc aggcgcggga gccgcctagg ctgctgggag tggtggtccg gccgcggaat  240
     175 ggagatcctg aaggagctag acgagtgcta cgagcgcttc agtcgcgaga cagacggggc  300
     177 gcagaagcgg cggatgctgc actgtgtgca gcgcgcgctg atccgcagcc aggagctggg  360
     179 cgacgagaag atccagatcg tgagccagat ggtggagctg gtggagaacc gcacgcggca  420
     181 ggtggacagc cacgtggagc tgttcgaggc gcagcaggag ctgggcgaca cagcgggcaa  480
     183 cagcggcaag gctggcgcgg acaggcccaa aggcgaggcg gcagcgcagg ctgacaagcc  540
     185 caacagcaag cgctcacggc ggcagcgcaa caacgagaac cgtgagaacg cgtccagcaa  600
     187 ccacgaccac gacgacggcg cctcgggcac acccaaggag aagaaggcca agacctccaa  660
     189 gaagaagaag cgctccaagg ccaaggcgga gcgagaggcg tcccctgccg acctccccat  720
     191 cgaccccaac gaacccacgt actgtctgtg caaccaggtc tcctatgggg agatgatcgg  780
     193 ctgcgacaac gacgagtgcc ccatcgagtg gttccacttc tcgtgcgtgg ggctcaatca  840
     195 taaacccaag ggcaagt                                                  857
     198 <210> SEQ ID NO: 5
     199 <211> LENGTH: 279
     200 <212> TYPE: PRT
     201 <213> ORGANISM: Homo sapiens
W--> 202 <400> SEQUENCE: 5
     203 Met Leu Ser Pro Ala Asn Gly Glu Gln Leu His Leu Val Asn Tyr Val
     204 1               5                   10                  15
     206 Glu Asp Tyr Leu Asp Ser Ile Glu Ser Leu Pro Phe Asp Leu Gln Arg
     207             20                  25                  30
     209 Asn Val Ser Leu Met Arg Glu Ile Asp Ala Lys Tyr Gln Glu Ile Leu
     210             35                  40                  45
     212 Lys Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly
     213     50                  55                  60
     215 Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg
     216 65                  70                  75                  80
     218 Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val
     219             85                  90                  95
     221 Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu
     222             100                 105                 110
     224 Phe Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys
     225         115                 120                 125
     227 Val Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys
     228     130                 135                 140
     230 Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu
     231 145                 150                 155                 160
     233 Asn Ala Ser Ser Asn His Asp His Asp Asp Gly Ala Ser Gly Thr Pro
     234             165                 170                 175
     236 Lys Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Arg Ser Lys Ala
     237             180                 185                 190
     239 Lys Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn
     240         195                 200                 205
     242 Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile
     243         210                 215                 220
```

```
    245 Gly Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys
    246 225                 230                 235                 240
    248 Val Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys
    249                     245                 250                 255
    251 Arg Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys
    252                     260                 265                 270
    254 Lys Glu Arg Ala Tyr Asn Arg
    255             275
    258 <210> SEQ ID NO: 6
    259 <211> LENGTH: 210
    260 <212> TYPE: PRT
    261 <213> ORGANISM: Homo sapiens
W--> 262 <220> FEATURE:
W--> 263 <400> SEQUENCE: 6
    264 Met Leu His Cys Val Gln Arg Ala Leu Ile Arg Ser Gln Glu Leu Gly
    265 1               5                   10                  15
    267 Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val Glu Leu Val Glu Asn
    268                 20                  25                  30
    270 Arg Thr Arg Gln Val Asp Ser His Val Glu Leu Phe Glu Ala Gln Gln
    271             35                  40                  45
    273 Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys Val Gly Ala Asp Arg
    274         50                  55                  60
    276 Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys Pro Asn Ser Lys Arg
    277 65                  70                  75                  80
    279 Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu Asn Ala Ser Ser Asn
    280                 85                  90                  95
    282 His Asp His Asp Asp Gly Ala Ser Gly Thr Pro Lys Glu Lys Lys Ala
    283             100                 105                 110
    285 Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala Lys Ala Glu Arg Glu
    286         115                 120                 125
    288 Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn Glu Pro Thr Tyr Cys
    289     130                 135                 140
    291 Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile Gly Cys Asp Asn Asp
    292 145                 150                 155                 160
    294 Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys Val Gly Leu Asn His
    295                 165                 170                 175
    297 Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys Arg Gly Glu Asn Glu
    298             180                 185                 190
    300 Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys Lys Glu Arg Ala Tyr
    301         195                 200                 205
    303 Asn Arg
    304     210
    307 <210> SEQ ID NO: 7
    308 <211> LENGTH: 235
    309 <212> TYPE: PRT
    310 <213> ORGANISM: Homo sapiens
W--> 311 <400> SEQUENCE: 7
    312 Met Glu Ile Leu Lys Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg
    313 1               5                   10                  15
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/451,739D

DATE: 11/09/2001
TIME: 11:14:22

Input Set : A:\#703518v1 -DECEMBER 8 REVISED SEQUENCE LISTING NDH.txt
Output Set: N:\CRF3\11092001\I451739D.raw

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315 Glu Thr Asp Gly Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg
316           20              25              30
318 Ala Leu Ile Arg Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val
319         35              40              45
321 Ser Gln Met Val Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser
322     50              55              60
324 His Val Glu Leu Phe Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly
325 65              70              75              80
327 Asn Ser Gly Lys Val Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala
328             85              90              95
330 Gln Ser Asp Lys Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn
331             100             105             110
333 Glu Asn Arg Glu Asn Ala Ser Ser Asn His Asp His Asp Asp Gly Ala
334         115             120             125
336 Ser Gly Thr Pro Lys Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Lys
337     130             135             140
339 Arg Ser Lys Ala Lys Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro
340 145             150             155             160
342 Ile Asp Pro Asn Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr
343             165             170             175
345 Gly Glu Met Ile Gly Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe
346             180             185             190
348 His Phe Ser Cys Val Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr
349         195             200             205
351 Cys Pro Lys Cys Arg Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu
352     210             215             220
354 Glu Lys Ser Lys Lys Glu Arg Ala Tyr Asn Arg
355 225             230             235
358 <210> SEQ ID NO: 8
359 <211> LENGTH: 772
360 <212> TYPE: DNA
361 <213> ORGANISM: Homo sapiens
362 <221> NAME/KEY: CDS
363 <222> LOCATION: 689,714
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W--> 364 <400> SEQUENCE: 8

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365 aaagcgttct cggcggcagc gcaacaacta gaaccgtgag aacgcgtcca gcaaccgcga     60
367 cccacgacga cgtcacctcg ggcacgccca aggagaagaa agcccagacc tctaagaaga    120
369 agcagggctc catggccaag gcgtagcggc aggcgtcccc cgcagacctc cccatcgacc    180
371 ccagcgagcc ctcctactgg gagatgatcc gctgcgacaa cgaatgcccc atcgagtggt    240
373 tccgcttctc gtgtgtgagt ctcaaccata aaccaaagcg caagtggtac tgttccagat    300
375 gccggggaaa gaacgatggg caaagccctt gagaagtcca gaaaaaaaac agggcttata    360
377 acaggtagtt tggggacatg cgtctaatag tgaggagaac aaaataagcc agtgtgttga    420
379 ttacattgcc acctttgctg aggtgcagga agtgtaaaat gtatattttt aaagaatgtt    480
381 gttagaggcc gggcgcggtg gctcacgcct gtaatcccag cactttggga ggccgaggcg    540
383 gtcggatcac gaggtcagga gatcgagacc atcctggcta acacggtgaa accccgtctc    600
385 tactaaaaat tcaaaaaaaa aattagctgg gcgtggtggc gggcgcctgt agtcccagct    660
```

W--> 387 attcgggagg ctgaggcagg agaatgg(ch)t gaacctggga ggtggagctt gca(h)tgagcc   720

```
389 aaggtcgcgc cactgcactc cagcctgggc gacagagcga gactccatct ta               772
392 <210> SEQ ID NO: 9
```

VERIFICATION SUMMARY   DATE: 11/09/2001
PATENT APPLICATION: US/09/451,739D   TIME: 11:14:23

Input Set : A:\#703518v1 -DECEMBER 8 REVISED SEQUENCE LISTING NDH.txt
Output Set: N:\CRF3\11092001\I451739D.raw

```
L:25 M:283 W: Missing Blank Line separator, <220> field identifier
L:29 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:87 M:283 W: Missing Blank Line separator, <400> field identifier
L:133 M:283 W: Missing Blank Line separator, <220> field identifier
L:134 M:283 W: Missing Blank Line separator, <400> field identifier
L:166 M:283 W: Missing Blank Line separator, <400> field identifier
L:202 M:283 W: Missing Blank Line separator, <400> field identifier
L:262 M:283 W: Missing Blank Line separator, <220> field identifier
L:263 M:283 W: Missing Blank Line separator, <400> field identifier
L:311 M:283 W: Missing Blank Line separator, <400> field identifier
L:364 M:283 W: Missing Blank Line separator, <400> field identifier
L:387 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:387 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:396 M:283 W: Missing Blank Line separator, <400> field identifier
L:404 M:283 W: Missing Blank Line separator, <400> field identifier
L:412 M:283 W: Missing Blank Line separator, <400> field identifier
L:420 M:283 W: Missing Blank Line separator, <400> field identifier
L:428 M:283 W: Missing Blank Line separator, <400> field identifier
L:436 M:283 W: Missing Blank Line separator, <400> field identifier
L:446 M:283 W: Missing Blank Line separator, <400> field identifier
L:501 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:501 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:505 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:505 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:509 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:509 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:511 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:511 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:513 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:513 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:520 M:283 W: Missing Blank Line separator, <400> field identifier
L:622 M:283 W: Missing Blank Line separator, <400> field identifier
L:630 M:283 W: Missing Blank Line separator, <400> field identifier
L:638 M:283 W: Missing Blank Line separator, <400> field identifier
```

Errored (handwritten annotation)

Must enumerate n's

<210> 15
<211> 2030
<212> DNA
<213> Homo sapiens
<221> CDS
<222> 1628, 1752, 1758, 1769, 1789, 1873, 1908, 1915, 1933, 1970, 1976,2022
<400> 15

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ctgccttcga gcctgccatt gaaatgcaaa agtctgttcc aaataaagcc ttggaattga 180

agaatgaaca aacattgaga gcagatgaga tactcccatc agaatccaaa caaaaggact 240

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Errored: must enumerate n's.